

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: February 9, 2005, 08:45:53 ; Search time 0.001 Seconds  
("without alignments")  
749.952 Million cell updates/sec

Title: US-09-824-134-1  
Perfect score: 186  
Sequence: 1 TGGAGAAGGCTGGCTCGTCA.....CCTGCCAGATGAACCTGTG

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2016 residues

Total number of hits satisfying Chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : US09758003.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Description            |
|------------|-------|-------------|------------------------|
|            |       | Length      | DB ID                  |
| 1          | 15.6  | 8.4         | Sequence 1, Appli      |
| c 2        | 14    | 7.5         | 2016 1 US-09-758-003-1 |
|            |       |             | Sequence 1, Appli      |

## ALIGNMENTS

RESULT 1  
US-09-758-003-1  
Sequence 1, Application US/09758003

GENERAL INFORMATION:  
APPLICANT: BAICHWAL, VIJAY R  
HUANG, JIANNING  
HSU, HAILING  
GOEDDEL, DAVID V

TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,003  
FILING DATE: 09-Jan-2001  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T95-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-3341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:

FILING DATE: 09-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/132,118  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T95-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2016 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: Linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2013  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-758-003-1  
Query Match 8.4%; Score 15.6%; DB 1; Length 2016;  
Best Local Similarity 63.2%; Pred. No. 0;  
Matches 24; Mismatches 0; Indels 0; Gaps 0;  
Qy 575 CACTGAGAACTGGAGAACAGAGAAGGAAACCA 612  
Db 1197 CAGACGAAATGTGGTTACACAGAGGAAAGGA 1234  
RESULT 2  
US-09-758-003-1/c  
Sequence 1, Application US/09758003  
GENERAL INFORMATION:  
APPLICANT: BAICHWAL, VIJAY R  
HUANG, JIANNING  
HSU, HAILING  
GOEDDEL, DAVID V  
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,003  
FILING DATE: 09-Jan-2001  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T95-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-3341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2016 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2013  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
us-09-758-003-1

---

Query Match 7.5%; Score 14; DB 1; Length 2016;  
Best Local Similarity 60.5%; Pred. No 0;  
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

|    |     |                                      |     |
|----|-----|--------------------------------------|-----|
| Qy | 499 | CTCAAAGTCTGAGACCAAGATCGACAGCATCGAGGA | 536 |
| Db | 87  | CCCAAAGCTCCGGTGTCAAGTTCTGACTCTCAGGA  | 50  |

Search completed: February 9, 2005, 08:45:53  
Job time : 0.001 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_p1plus\_n2p model

Run on: February 9, 2005, 08:56:35 ; Search time 0.001 Seconds  
 (without alignments)  
 2282.742 Million cell updates/sec

Title: US-09-824-134-1  
 Perfect score: 3092  
 Sequence: 1 GTGATCAGGCCACGGAGTG.....ACAAAAAA.....AAAAA 1701

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 1 seqs, 671 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Command line parameters:  
 -MODEL=frame + n2p.model1 - DEV=80f - Q=US09824134.seq -DB=US09758003.ped  
 -PREFIX=p1o -OUT=US09824134-1.n2p ALIGN-MINMATCH=0.1 -LOOPEXT=0  
 -UNITS=bits -START=1 -END=1 - MATRIX=blosum62 -TRANS=human40\_cdi -LIST=45  
 -DOALIGN=1 -N0 -THR SCORB=pct -THR MAX=100 -THR MIN=-100  
 -ALIGN=15 -MAXLEN=500 -MINLEN=0 -NCPO=6  
 -NO\_XLIPXY -NEC SCORES=ext -HEAPSIZEx=500 -NCPD=0  
 -NO\_XLIPXY -NEC SCORES=ext -LONGLOG -THREADS=1 -XGAPLEN=10 -XGABEXT=0.5 -FGAPPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : US09758003.ped:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Description       | Length | DB ID             |
|------------|-------|-------------|-------------------|--------|-------------------|
| 1          | 111.5 | 3.6         | Sequence 2, Appli | 671    | 1 US-09-758-003-2 |
| c          | 2 47  | 1.5         | Sequence 2, Appli | 671    | 1 US-09-758-003-2 |

#### ALIGNMENTS

RESULT 1  
 US-09-758-003-2  
 ; Sequence 2, Application US/09758003

; GENERAL INFORMATION:  
 ; APPLICANT: BAICHWAL, VIJAY R

HUANG, JIANNING  
 HSU, HAILING

GOEDDEL, DAVID V

TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS

NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/758,003  
 FILING DATE: 09-Jan-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/132,118  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T95-006-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 671 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-758-003-2

Alignment Scores:  
 Pred. No.: 0 Length: 671  
 Score: 111.50 Matches: 28  
 Percent Similarity: 61.04% Conservative: 19  
 Best Local Similarity: 36.36% Mismatches: 27  
 Query Match: 3.61\$ Indels: 3  
 DB: 1 Gaps: 3

US-09-824-134-1 (1-1701) x US-09-758-003-2 (1-671)

Qy 454 ATATGTGATAATGTGGGAAAGATGGAGAGCTCGTCGCTCAAAGTCCTAGAC 513  
 Db 590 IleArgLeuGlnLeuGlySerGluAspGlyLeuLysGlnLysLeuGlyPheThrGln 609  
 Qy 514 ACCAAGATCGACAGCATCGAGGACAGATACCCCGAAAC--CTGACAGACGGTGTGCGG 570  
 Db 610 SerGlnLeuAspGlyLeuLysGlnLysLeuGlySerGlyAspGlyLeuLysGlnLysLeuGlySerValtryr 629  
 Qy 571 GAGTCACTGAGATCTGAAAGAACAGAGAG--GAGAACGCAACAGTGGCCACCTG 627  
 Db 630 GluMetLeuGlnLysTrpValMetArgGlnCAGGCTCTGC--CACATGAACTGTTGACCTGGTA 649  
 Qy 628 GTGGGGCTCTGAGCTGAAAGAACAGAGAG--GAGAACGCAACAGTGGCCACCTG 655  
 Db 650 AlaGlnLysLeuGlnCysSerArgIleLeuLeuSerLeuIle 666

RESULT 2  
 US-09-758-003-2  
 ; Sequence 2, Application US/09758003  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BAICHWAL, VIJAY R  
 HUANG, JIANNING  
 HSU, HAILING  
 GOEDDEL, DAVID V  
 TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS

NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/758,003  
 FILING DATE: 09-Jan-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/132,118  
 FILING DATE: Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSNAN, RICHARD A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T95-006-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 341-4342  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 671 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-758-003-2

## Alignment Scores:

|    |      |  |
|----|------|--|
| Qy | 1455 | CTCAATTCCCTCCTCG---CAAATCATCTG-----CCC 1426                      |
| Db | 354  | VaiGluGluSerIrpPhalaProSerIrpGluAsnGluProSer 373                 |
| Qy | 1425 | CTACTTGGAGTCTCAGAGGAGACTCAACTC--ACACAGGGCAAGAGCTGGCCA 1369       |
| Db | 374  | LeuGlnSerLysIleGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArg 393 |
| Qy | 1368 | CGGCAACAGGTCTCCCAACCCCCACCCAGCCAT-----GCCTCTCCACAC 1318          |
| Db | 394  | GlnThrLysGlnGlnProArgGlnAlaTyrAsnArgGluGluGluArgArgArg 413       |
| Qy | 1317 | AGCACCCCCGTAACCTGTCGCTGCACTGTGCC-----GTTGCCCTCAA 1270            |
| Db | 414  | ArgValSerHisAspProHeAlaGlnArgProTyroGluAsnDheGlnAsnThrGlu 433    |
| Qy | 1269 | GGAATGGACAAAAAACATCCTTCTGCCAATCTGAGGG--GCAGCAGAACGCCACAGT 1213   |
| Db | 434  | GlyLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer 453 |
| Qy | 1212 | GGTGAGCA-----TGGGTCTGTGANGATGGCGG----- 1180                      |
| Db | 454  | GlyIleThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyIleTyrSerSerHisGly 473 |
| Qy | 1179 | --GGTCAAACTCCAGTCCTCCACCTCTCTGCTCGGATTCTGGCTCTGAGC 1123          |
| Db | 474  | PhedLysThrArgProLeuAspProlGlyThrAla-----GlyProArgVal 488         |
| Qy | 1122 | TGGTCTCCCTCCGCTGTGGAAGTAAAGCTGTCATCT-GCACAGATTCCT----- 1070      |
| Db | 489  | TryptArgProleProSerHisMetProSerLeuHisAsnIleProValProGluThr 508   |

Page 1

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.  
Copyright

CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTY: USA

*M* protein - nucleic search, using frame\_plus\_p2n model

on : February 9, 2005, 09:04:15 ; Search time 0.001 Seconds  
 (without alignment) ; 1032.192 Million cell updates/sec

title: US-09-824-134-2  
perfect score: 1302  
sequence: 1 VNQAPECRFGGIGLGPUGKR..... RSGANSPMNSNDASTSEAS 256

| Scoring table: | Blossom <sub>2</sub> | Xgapop | Xgapext | 0.5 |
|----------------|----------------------|--------|---------|-----|
| Xgapop         | 10.0                 | -      | Xgapext | 0.5 |
| Ygapop         | 10.0                 | -      | Ygapext | 0.5 |
| Fgapop         | 6.0                  | -      | Fgapext | 7.0 |
| Delop          | 6.0                  | -      | Delext  | 7.0 |

searched : 1 seqs, 2016 residues  
total number of hits satisfying chosen parameters: 2

minimum DB seq length: 0  
maximum DB seq length: 200000000

OBEL-processing: Maximum Match 100%  
Listning first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

Documentation  
Query : [??](#)  
result : [??](#)

Sequence 1, App1  
Comments 1, App1

ALIGNMENTS

RESULTS 1

Sequence 1, Application US/09758003  
GENERAL INFORMATION:

AFFILIATE: *UNIVERSITY OF TORONTO*  
HUAJUAN, JIANNING  
HSU, HAILING

**TITLE OF INVENTION:** RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
COUNSEL FOR INTELLECTUAL PROPERTY  
ATTORNEYS AT LAW

NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENSE DRIVE  
 CITY: HILLISBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/758,003  
 FILING DATE: 09-Jan-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/132,118  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A.  
 REGISTRATION NUMBER: 3,6,627  
 REFERENCE/DOCKET NUMBER: T95-006-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEX/FAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2016 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..2013  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-758-003-1

Alignment Scores:  
 Pred. No.: 0 Length: 20  
 Score: 48.00 Matches: 26  
 Percent Similarity: 50.00% Conservative: 8  
 Best Local Similarity: 38.24% Mismatches: 26  
 Query Match: 3.69% Indels: 8  
 DB: 1 Gaps: 5

US-09-824-134-2 (1-256) x US-09-758-003-1 (1-2016)

|    |  |   |  |
|----|--|---|--|
| Qy | 42 ArgProlLeuAlaAspProAlaMetAspProPheLeuValLeu | Y | 1257 AGGGTCATGGAGAACCTCGG--TCTCCCTTCTCTCCTC-     |
| Db |  |   |  |
| Qy | 62 SerLeuSerSerGluLeuThrGluLeuLysPhe-----      | Y | 1209 CACATTCTGTCTGGCTGCTGTTGCTCATGGCTGGCTCAATT   |
| Db |  |   |  |
| Qy | 80 ValIleArgLysLeuGlu---ArgValGinSerGlyLeuAsp  | Y | 1149 GTCGCTTCCTCTGGAGTTACTCTGAGGGCTGGCTGGCTCAATT |
| Db |  |   |  |
| Qy | 99 GluGlnAsnAspLeuGluProGly 106                | Y | 1089 ---CAGGGAAAGGAGAAAACCAGGA 1069              |
| Db |  |   |  |

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 09:01:06 ; Search time 0.001 Seconds  
 (without alignments)  
 77.836 Million cell updates/sec

Title: US-09-824-134-2  
 Perfect score: 593  
 Sequence: 1 FPLGAAARGAAPGEEDLCAAF.....QEVOQARDLQNRSGAMSPMS 116

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 671 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing First 45 summaries  
 Database : US09758003.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Query Score | Match Length | DB ID | Description                       |
|------------|-------------|--------------|-------|-----------------------------------|
| 1          | 111.5       | 18.8         | 671 1 | US-09-758-003-2 Sequence 2, Appli |

#### ALIGNMENTS

| RESULT 1 | US-09-758-003-2 | Sequence 2, Application US/09758003 | GENERAL INFORMATION:   | ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP      |
|----------|-----------------|-------------------------------------|--|--|
|          |                 |                                     | APPLICANT: BAICHWAL, VILJAY R  | STREET: 75 DENISE DRIVE                        |
|          |                 |                                     | HUANG, JIANNING  | CITY: HILLSBOROUGH                             |
|          |                 |                                     | HSU, HAILING   | STATE: CALIFORNIA                              |
|          |                 |                                     | GODEDEL, DAVID V   | COUNTRY: USA                                   |
|          |                 |                                     | TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS | ZIP: 94110                                     |
|          |                 |                                     | NUMBER OF SEQUENCES: 2   | COMPUTER READABLE FORM:                        |
|          |                 |                                     | CORRESPONDENCE ADDRESS   | MEDIUM TYPE: Floppy disk                       |
|          |                 |                                     | STREET: 75 DENISE DRIVE  | COMPUTER: IBM PC compatible                    |
|          |                 |                                     | CITY: HILLSBOROUGH   | OPERATING SYSTEM: PC-DOS/MS-DOS                |
|          |                 |                                     | STATE: CALIFORNIA  | SOFTWARE: PatentIn Release #1.0, Version #1.30 |
|          |                 |                                     | COUNTRY: USA   | CURRENT APPLICATION DATA:                      |
|          |                 |                                     | ZIP: 94110   | APPLICATION NUMBER: US/09/758,003              |
|          |                 |                                     | COMPUTER READEABLE FORM:   | FILING DATE: 09-Jan-2001                       |

THIS PAGE LEFT BLANK